

MARCH 2002

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645

F A R M A C Y

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/960,738A

DATE: 02/26/2002

TIME: 13:59:55

Input Set : A:\032301.218.ST25.txt

Output Set: N:\CRF3\02262002\I960738A.raw

3 <110> APPLICANT: BATHE, Brigitte, et al.
 5 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE ppkK GENE
 7 <130> FILE REFERENCE: 032301 WD 218
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/960,738A
 C--> 9 <141> CURRENT FILING DATE: 2001-09-24
 9 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1239
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Corynebacterium glutamicum
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (237)..(1022)
 21 <223> OTHER INFORMATION:
 24 <400> SEQUENCE: 1
 25 ggccgaaggct cctgcaacctt attggcgata aaatcttcag ccaaagtatc tactatcg 60
 27 accggatcgat ctgtcaact ttgggtgtt gttgtatccc acaaaatttgtt gagttcagca 120
 29 cgcttatccc tgatacgtac agcggttaagc gtggcagttt ccgcggcgat ggcacgc 180
 31 tcattaaacgtt attgttgttc cataagacca tcatcggtt ttttttagaa aattgc ctg 239
 32 Met
 33 1
 35 cca aaa gcc gaa gta att tgt aca ctt ggg cgc atg act gag act gga 287
 36 Pro Lys Ala Glu Val Ile Cys Thr Leu Gly Arg Met Thr Glu Thr Gly
 37 5 10 15
 39 ttt gga att gat atc ggt ggc tcc ggc atc aaa ggc gcc cgc gtt aac 335
 40 Phe Gly Ile Asp Ile Gly Gly Ser Gly Ile Lys Gly Ala Arg Val Asn
 41 20 25 30
 43 ctt aag acc ggt gag ttt att gat gaa cgc ata aaa atc gcc acc cct 383
 44 Leu Lys Thr Gly Glu Phe Ile Asp Glu Arg Ile Lys Ile Ala Thr Pro
 45 35 40 45
 47 aag cca gca acc cca gag gct gtc gcc gaa gta gtc gca gag att att 431
 48 Lys Pro Ala Thr Pro Glu Ala Val Ala Glu Val Val Ala Glu Ile Ile
 49 50 55 60 65
 51 tct caa gcc gaa tgg gag ggt ccg gtc gga att acc ctg ccg tcg gtc 479
 52 Ser Gln Ala Glu Trp Glu Gly Pro Val Gly Ile Thr Leu Pro Ser Val
 53 70 75 80
 55 gtt cgc ggg cag atc gcg cta tcc gca gcc aac att gac aag tcc tgg 527
 56 Val Arg Gly Gln Ile Ala Leu Ser Ala Ala Asn Ile Asp Lys Ser Trp
 57 85 90 95
 59 atc ggc acc gat gtg cac gaa ctt ttt gac cgc cac cta aat ggc cga 575
 60 Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly Arg
 61 100 105 110

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63	gag	atc	acc	gtt	ctc	aat	gac	gca	gac	gcc	gcc	gca	atc	gcc	gaa	gca	623	
64	Glu	Ile	Thr	Val	Leu	Asn	Asp	Ala	Asp	Ala	Ala	Gly	Ile	Ala	Glu	Ala		
65	115				120						125							
66	acc	ttt	ggc	aac	cct	gcc	gca	cgc	gaa	ggc	gca	gtc	atc	ctg	ctg	acc	671	
67	Thr	Phe	Gly	Asn	Pro	Ala	Ala	Arg	Glu	Gly	Ala	Val	Ile	Leu	Leu	Thr		
68	130				135						140				145			
69	ctt	ggt	aca	ggt	att	gga	tcc	gca	tcc	ctt	gtg	gat	ggc	caa	ctg	tcc	719	
70	Leu	Gly	Thr	Gly	Ile	Gly	Ser	Ala	Phe	Leu	Val	Asp	Gly	Gln	Leu	Phe		
71	150				155						160							
72	ccc	aac	aca	gaa	ctc	ggt	cac	atg	atc	gtt	gac	ggc	gag	gaa	gca	gaa	767	
73	Pro	Asn	Thr	Glu	Leu	Gly	His	Met	Ile	Val	Asp	Gly	Glu	Ala	Glu			
74	165				170						175							
75	cac	ctt	gca	gca	gca	tcc	gtc	aaa	gaa	aac	gaa	gat	ctg	tca	tgg	aag	815	
76	His	Leu	Ala	Ala	Ala	Ser	Val	Lys	Glu	Asn	Glu	Asp	Leu	Ser	Trp	Lys		
77	180				185						190							
78	aaa	tgg	gcg	aag	cac	ctg	aac	aag	gtg	ctg	agc	gaa	tac	gag	aaa	ctt	863	
79	Lys	Trp	Ala	Lys	His	Leu	Asn	Lys	Val	Leu	Ser	Glu	Tyr	Glu	Lys	Leu		
80	195				200						205							
81	tcc	tcc	cca	tcc	gtc	tcc	atc	atc	ggt	ggc	gga	att	tcc	aga	aag	cac	911	
82	Phe	Ser	Pro	Ser	Val	Phe	Ile	Ile	Gly	Gly	Gly	Ile	Ser	Arg	Lys	His		
83	210				215						220				225			
84	gaa	aag	tgg	ctt	cca	ttg	atg	gag	cta	gac	act	gac	att	gtc	cca	gct	959	
85	Glu	Lys	Trp	Leu	Pro	Leu	Met	Glu	Leu	Asp	Thr	Asp	Ile	Val	Pro	Ala		
86	230				235						240							
87	91	gag	ctg	cgc	aat	cga	gcc	gga	atc	gta	gga	gct	gcc	atg	gca	gta	1007	
88	Glu	Leu	Arg	Asn	Arg	Ala	Gly	Ile	Val	Gly	Ala	Ala	Met	Ala	Val	Asn		
89	92	245			250						255							
90	caa	cac	ctc	acc	cca	taagttatcg	aaaggtgatt	tttgcccagg	gccttgattc								1062	
91	100	Gln	His	Leu	Thr	Pro												
92	101	260																
93	103	acaacgcacc	ttgctgttagg	aaaaacagggc	ccctttgtga	catcggcgta	gttggttcaac										1122	
94	105	tataatggaa	cgctgatcgt	ggacaagagt	taaccatgag	attgattcac	ccctttaagc										1182	
95	107	ctccaaagaa	gtagttgact	caacgcattt	cggcatttaa	aaaagccgag	agcaaat										1239	
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97	109	<211>	LENGTH: 262															
98	110	<212>	TYPE: PRT															
99	111	<213>	ORGANISM: Corynebacterium glutamicum															
100	112	<400>	SEQUENCE: 2															
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102	114	1				5				10				15				
103	115	Gly	Phe	Gly	Ile	Asp	Ile	Gly	Gly	Ser	Gly	Ile	Lys	Gly	Ala	Arg	Val	
104	116	121				20			25			30						
105	117	Asn	Leu	Lys	Thr	Gly	Glu	Phe	Ile	Asp	Glu	Arg	Ile	Lys	Ile	Ala	Thr	
106	118	122	1			35			40			45						
107	119	125	Met	Pro	Ala	Thr	Pro	Glu	Ala	Val	Ala	Glu	Val	Val	Ala	Glu	Ile	
108	120	126	50			55			60									
109	121	127	Ile	Ser	Gln	Ala	Glu	Trp	Glu	Gly	Pro	Val	Gly	Ile	Thr	Leu	Pro	Ser
110	122	128	65			70			75			80						
111	123	137	Val	Val	Arg	Gly	Gln	Ile	Ala	Leu	Ser	Ala	Ala	Asn	Ile	Asp	Lys	Ser

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138	85	90	95
141	Trp Ile Gly Thr Asp Val His Glu Leu Phe Asp Arg His Leu Asn Gly		
142	100	105	110
145	Arg Glu Ile Thr Val Leu Asn Asp Ala Asp Ala Gly Ile Ala Glu		
146	115	120	125
149	Ala Thr Phe Gly Asn Pro Ala Ala Arg Glu Gly Ala Val Ile Leu Leu		
150	130	135	140
153	Thr Leu Gly Thr Gly Ile Gly Ser Ala Phe Leu Val Asp Gly Gln Leu		
154	145	150	155
157	Phe Pro Asn Thr Glu Leu Gly His Met Ile Val Asp Gly Glu Glu Ala		
158	165	170	175
161	Glu His Leu Ala Ala Ser Val Lys Glu Asn Glu Asp Leu Ser Trp		
162	180	185	190
165	Lys Lys Trp Ala Lys His Leu Asn Lys Val Leu Ser Glu Tyr Glu Lys		
166	195	200	205
169	Leu Phe Ser Pro Ser Val Phe Ile Ile Gly Gly Ile Ser Arg Lys		
170	210	215	220
173	His Glu Lys Trp Leu Pro Leu Met Glu Leu Asp Thr Asp Ile Val Pro		
174	225	230	235
177	Ala Glu Leu Arg Asn Arg Ala Gly Ile Val Gly Ala Ala Met Ala Val		
178	245	250	255
181	Asn Gln His Leu Thr Pro		
182	260		

VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date